



SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> ADIP PROTEIN AND USE THEREOF

<130> 2144.0100000

<140> US 10/644,084

<141> 2003-08-20

<150> JP 2002-284263

<151> 2002-09-27

<160> 9

<170> PatentIn version 3.3

<210> 1

<211> 2692

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (80)..(1927)

<223> /note="afadin-and alpha-actinin-binding protein"

<400> 1

cgtaggagag tgacaggagc tggttgtaagc gtcgcagcac tgagccgcct cctcaggtat 60

cctggctctg gaacttgct atg gga gat tgg atg act gtg aca gat cca gtt 112
Met Gly Asp Trp Met Thr Val Thr Asp Pro Val
1 5 10

ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag 160
Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys
15 20 25

atg tct ccg tcc agt ttg tac tcc cag caa gtt ctg tgc tct tca gta 208
Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val
30 35 40

cct tta tcc aaa aac gtg cat ggt gtt ttc ggt gtc ttc tgc aca gga 256
Pro Leu Ser Lys Asn Val His Gly Val Phe Gly Val Phe Cys Thr Gly
45 50 55

gag aac att gaa caa agt att tcc tat ctt gat cag gag ctg acc acc 304
Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr
60 65 70 75

ttc ggg ttt cct tcc ttg tat gaa gaa tcc aaa agt aaa gag gca aag 352
Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys
80 85 90

aga gaa tta aat ata gtc gct gtt ctg aac tgt atg aac gag ctg ctc 400
Arg Glu Leu Asn Ile Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu
95 100 105

gtg ctt cag cgg aag aac ctg ctg gcc cag gag agc gtg gag aca cag 448

Val	Leu	Gln	Arg	Lys	Asn	Leu	Leu	Ala	Gln	Glu	Ser	Val	Glu	Thr	Gln	
		110					115					120				
aac	ttg	aag	ctg	ggc	agt	gac	atg	gac	cac	ctg	cag	agc	tgc	tac	gcc	496
Asn	Leu	Lys	Leu	Gly	Ser	Asp	Met	Asp	His	Leu	Gln	Ser	Cys	Tyr	Ala	
	125					130					135					
aaa	ctt	aag	gag	cag	ttg	gaa	acg	tcc	agg	cgg	gag	atg	atc	ggg	ctt	544
Lys	Leu	Lys	Glu	Gln	Leu	Glu	Thr	Ser	Arg	Arg	Glu	Met	Ile	Gly	Leu	
140					145					150					155	
caa	gag	aga	gac	agg	cag	ctg	cag	tgc	aag	aac	agg	agt	ttg	cat	cag	592
Gln	Glu	Arg	Asp	Arg	Gln	Leu	Gln	Cys	Lys	Asn	Arg	Ser	Leu	His	Gln	
				160					165					170		
ctc	ctg	aag	aat	gag	aaa	gat	gag	gta	caa	aaa	tta	caa	aat	atc	ata	640
Leu	Leu	Lys	Asn	Glu	Lys	Asp	Glu	Val	Gln	Lys	Leu	Gln	Asn	Ile	Ile	
			175					180					185			
gcc	agc	cgg	gct	act	cag	tat	aat	cat	gat	gtg	aag	agg	aag	gag	cgt	688
Ala	Ser	Arg	Ala	Thr	Gln	Tyr	Asn	His	Asp	Val	Lys	Arg	Lys	Glu	Arg	
		190					195					200				
gaa	tat	aat	aag	cta	aag	gag	cgc	ctg	cat	cag	ctc	gtt	atg	aac	aag	736
Glu	Tyr	Asn	Lys	Leu	Lys	Glu	Arg	Leu	His	Gln	Leu	Val	Met	Asn	Lys	
	205					210					215					
aag	gat	aaa	aac	ata	gcc	atg	gat	gtt	tta	aat	tat	gtg	ggg	cga	gct	784
Lys	Asp	Lys	Asn	Ile	Ala	Met	Asp	Val	Leu	Asn	Tyr	Val	Gly	Arg	Ala	
220					225					230					235	
gat	ggc	aaa	cga	ggc	tca	tgg	agg	act	gac	aaa	aca	gaa	gcc	agg	aat	832
Asp	Gly	Lys	Arg	Gly	Ser	Trp	Arg	Thr	Asp	Lys	Thr	Glu	Ala	Arg	Asn	
				240					245					250		
gaa	gat	gag	atg	tac	aaa	att	ctg	ttg	aat	gat	tat	gag	tac	cgc	cag	880
Glu	Asp	Glu	Met	Tyr	Lys	Ile	Leu	Leu	Asn	Asp	Tyr	Glu	Tyr	Arg	Gln	
			255				260						265			
aag	cag	atc	ctg	atg	gag	aac	gcg	gag	ctg	aag	aag	gtc	ctc	cag	cag	928
Lys	Gln	Ile	Leu	Met	Glu	Asn	Ala	Glu	Leu	Lys	Lys	Val	Leu	Gln	Gln	
		270					275					280				
atg	aag	aag	gag	atg	atc	tct	ctc	ctg	tct	cct	cag	aag	aag	aag	ccc	976
Met	Lys	Lys	Glu	Met	Ile	Ser	Leu	Leu	Ser	Pro	Gln	Lys	Lys	Lys	Pro	
	285					290					295					
agg	gaa	aga	gca	gag	gac	ggc	aca	ggc	act	gtt	gct	atc	tcc	gat	ata	1024
Arg	Glu	Arg	Ala	Glu	Asp	Gly	Thr	Gly	Thr	Val	Ala	Ile	Ser	Asp	Ile	
300					305					310					315	
gaa	gat	gac	tct	ggg	gaa	ctg	agc	aga	gac	agc	gtg	tgg	ggc	ctt	tcc	1072
Glu	Asp	Asp	Ser	Gly	Glu	Leu	Ser	Arg	Asp	Ser	Val	Trp	Gly	Leu	Ser	
				320					325					330		
tgt	gac	act	gtg	aga	gag	cag	ctg	aca	aac	agc	atc	agg	aaa	cag	tgg	1120
Cys	Asp	Thr	Val	Arg	Glu	Gln	Leu	Thr	Asn	Ser	Ile	Arg	Lys	Gln	Trp	
			335				340						345			
aga	att	ttg	aaa	agt	cat	gta	gaa	aaa	ctc	gat	aac	caa	gct	tcg	aag	1168
Arg	Ile	Leu	Lys	Ser	His	Val	Glu	Lys	Leu	Asp	Asn	Gln	Ala	Ser	Lys	

350	355	360	
gta cac tca gag ggc ctt aat gag gag gac gtc atc tca cga caa gac Val His Ser Glu Gly Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp 365 370 375			1216
cat gag caa gag act gag aaa ctg gag ctg gag att gag cgg tgt aaa His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys 380 385 390 395			1264
gag atg atc aag gct cag cag cag ctc tta cag cag cag ctg gcc acc Glu Met Ile Lys Ala Gln Gln Gln Leu Leu Gln Gln Glu Ala Thr 400 405 410			1312
acg tgt gat gat gac acc acc tca ctg ttg cga gac tgt tac ttg ctg Thr Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu 415 420 425			1360
gaa gaa aag gaa cgc ctt aaa gaa gag tgg acc ctt ttt aaa gag caa Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln 430 435 440			1408
aaa aag aat ttt gag aga gaa agg cga agc ttt aca gaa gct gcc att Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile 445 450 455			1456
cga ttg ggg ttg gag aga aag gcg ttt gaa gaa gag cga gcc agc tgg Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp 460 465 470 475			1504
gta aag cag cag ttt tta aac atg acg aac ttt gac cac cag aac tca Val Lys Gln Gln Phe Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser 480 485 490			1552
gaa aat gtg aaa ctt ttc agt gcc ttc tca gga agt tct gat cca gac Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp 495 500 505			1600
aat ctt ata gtc cac tca cgg cca cgg caa aag aag cta cac agt gtg Asn Leu Ile Val His Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val 510 515 520			1648
gct aat ggg gtg cca gct tgc aca tca aaa ctg act aaa tct ctt cct Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro 525 530 535			1696
gcc tca cct tct act tca gac ttt cgc cag aca cat tca tgt gtg tct Ala Ser Pro Ser Thr Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser 540 545 550 555			1744
gaa cac agt tcc atc agt gtg ctg aat ata act cct gaa gaa agt aaa Glu His Ser Ser Ile Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys 560 565 570			1792
cca agt gag gtt gca aga gaa agc acg gat cag aag tgg agc gtg cag Pro Ser Glu Val Ala Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln 575 580 585			1840
tcg agg ccc agc tcg cgg gag ggg tgc tac agc gga tgc tcc tcg gcc Ser Arg Pro Ser Ser Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala 590 595 600			1888

ttc agg agc gct cac ggg gac cga gat gac tta cct taa atgtgcgggc 1937
 Phe Arg Ser Ala His Gly Asp Arg Asp Asp Leu Pro
 605 610 615
 tgcagtgtctg ttcccagatg tgcgctagag gagttgacac aggggtgtagc ataaagtcag 1997
 tcgtctaact taagatgctc agagttgttt gtttggaactt cgctgtcttc ccccaaagag 2057
 ctgaaatgct aagctactta aaaggatgca aagcttttgtt tgtgtgttag taacagaagc 2117
 ccctggctct gtgactgcag gaatgcatgg cgtttggaatg gaaacagaag cgctggaatg 2177
 attgcctcgc caggtagcga gaagagcact tttagggact ggctcctgta aacattaaat 2237
 attcgtccca agtgtgggtg gcattggaag tgtagccttt acttgaatgt atactgtaga 2297
 tttttaacaa agcagggttct atatttatta tgttttagtgt gattttggga ttacctcttt 2357
 catatgtttt gtgtctgtac ataaatatac atgactatgt taagaggctt taaggtttaa 2417
 aaacttcaca ccatgcttga gtatagcatt tcatgccaat taaaatgttt tcagtggcat 2477
 ggtgtttaca gaggttagga ccactgccac atgacagtta agactttatt tttaagccat 2537
 ctgggcaata aaaattcaaa gcccttcat aagctgagtt cagataacta gaactactaa 2597
 cgttacattt ttgagatttt taaagcattg tattttattt tatatatgtg aatgttataa 2657
 tttctaagag gaatattgat tatggagtaa tgggg 2692

<210> 2
 <211> 615
 <212> PRT
 <213> Mus musculus

<400> 2

Met Gly Asp Trp Met Thr Val Thr Asp Pro Val Leu Cys Thr Glu Asn
 1 5 10 15

Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser
 20 25 30

Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val Pro Leu Ser Lys Asn
 35 40 45

Val His Gly Val Phe Gly Val Phe Cys Thr Gly Glu Asn Ile Glu Gln
 50 55 60

Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
 65 70 75 80

Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Asn Ile
 85 90 95

Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
 100 105 110

Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
 115 120 125

Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
 130 135 140

Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg
 145 150 155 160

Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln Leu Leu Lys Asn Glu
 165 170 175

Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
 180 185 190

Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
 195 200 205

Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
 210 215 220

Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly
 225 230 235 240

Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
 245 250 255

Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met
 260 265 270

Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met
 275 280 285

Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro Arg Glu Arg Ala Glu
 290 295 300

Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile Glu Asp Asp Ser Gly
 305 310 315 320

Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser Cys Asp Thr Val Arg
 325 330 335

Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
 340 345 350

His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
 355 360 365

Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
 370 375 380

Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
 385 390 395 400

Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Thr Cys Asp Asp Asp
 405 410 415

Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
 420 425 430

Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
 435 440 445

Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
 450 455 460

Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe
 465 470 475 480

Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu
 485 490 495

Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
 500 505 510

Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val Ala Asn Gly Val Pro
 515 520 525

Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr
 530 535 540

Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser Glu His Ser Ser Ile
 545 550 555 560

Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys Pro Ser Glu Val Ala
 565 570 575

Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln Ser Arg Pro Ser Ser
580 585 590

Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala Phe Arg Ser Ala His
595 600 605

Gly Asp Arg Asp Asp Leu Pro
610 615

```
<210> 3
<211> 3195
<212> DNA
<213> Rattus norvegicus
```

```
<220>
<221> CDS
<222> (79) .. (1920)
```

```
<220>
<221> misc_feature
<222> (2422)..(2422)
<223> "n"=any one base of a, t, c, or g
```

<400> 3																	
gtaggagagt gacaggagct gttgtgcatg ccccagcact gaactgcctt ctcagggacc																	60
ctggctctgg gactggct atg gga gat tgg atg act gtt aca gat cca gtt																	111
Met Gly Asp Trp Met Thr Val Thr Asp Pro Val																	
1 5 10																	
ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag																	159
Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys																	
15 20 25																	
atg tct ccg tca agt tta tac tcg cag caa gta ctg tgc tct gca aca																	207
Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ala Thr																	
30 35 40																	
cct tta tcc aag aat gtg cat ggt gtt ttc agt gcc ttc tgc aca gga																	255
Pro Leu Ser Lys Asn Val His Gly Val Phe Ser Ala Phe Cys Thr Gly																	
45 50 55																	
gag aac atc gaa cag agt att tcg tat ctt gat cag gaa ctg act acc																	303
Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr																	
60 65 70 75																	
ttc ggt ttc cct tcc ttg tat gaa gaa tcc aaa agt aag gag gcg aag																	351
Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys																	
80 85 90																	
cga gag tta agt ata gtt gct ctt ctg aac tgc atg aat gag ctg ctt																	399
Arg Glu Leu Ser Ile Val Ala Leu Leu Asn Cys Met Asn Glu Leu Leu																	
95 100 105																	
gtg ctt cag cgg aag aac ctc ctg gcc cag gaa agc gtg gag aca cag																	447
Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln																	
110 115 120																	

aat	ctg	aag	ctg	ggc	agt	gac	atg	gac	cac	ctg	cag	agc	tgc	tac	gcc	495
Asn	Leu	Lys	Leu	Gly	Ser	Asp	Met	Asp	His	Leu	Gln	Ser	Cys	Tyr	Ala	
125						130					135					
aaa	ctt	aag	gaa	cag	ttg	gag	gcc	tcc	agg	cga	gag	atg	atc	agc	ctt	543
Lys	Leu	Lys	Glu	Gln	Leu	Glu	Ala	Ser	Arg	Arg	Glu	Met	Ile	Ser	Leu	
140					145					150					155	
cag	gag	aga	gac	aga	cag	cta	cag	tgc	aaa	aac	agg	aat	ttg	cat	cag	591
Gln	Glu	Arg	Asp	Arg	Gln	Leu	Gln	Cys	Lys	Asn	Arg	Asn	Leu	His	Gln	
				160						165					170	
ctc	ctg	aaa	aac	gag	aaa	gaa	gag	gta	caa	aaa	tta	caa	aat	atc	ata	639
Leu	Leu	Lys	Asn	Glu	Lys	Glu	Glu	Val	Gln	Lys	Leu	Gln	Asn	Ile	Ile	
			175					180						185		
gcc	agt	cgg	gct	act	cag	tat	aat	cat	gat	gtg	aag	aga	aag	gag	cgg	687
Ala	Ser	Arg	Ala	Thr	Gln	Tyr	Asn	His	Asp	Val	Lys	Arg	Lys	Glu	Arg	
		190					195					200				
gag	tac	aat	aaa	ctg	aag	gag	cgt	ctg	cat	cag	ctt	gtt	atg	aac	aag	735
Glu	Tyr	Asn	Lys	Leu	Lys	Glu	Arg	Leu	His	Gln	Leu	Val	Met	Asn	Lys	
	205					210					215					
aag	gat	aaa	aat	ata	gcc	atg	gac	gtt	tta	aat	tac	gtg	ggc	cga	gtg	783
Lys	Asp	Lys	Asn	Ile	Ala	Met	Asp	Val	Leu	Asn	Tyr	Val	Gly	Arg	Val	
220					225					230					235	
gat	gga	aag	cga	ggc	tcc	tgg	agg	act	gat	aaa	aca	gaa	gcc	agg	aat	831
Asp	Gly	Lys	Arg	Gly	Ser	Trp	Arg	Thr	Asp	Lys	Thr	Glu	Ala	Arg	Asn	
				240					245					250		
gaa	gat	gaa	atg	tac	aaa	att	ctg	ctg	aat	gat	tat	gag	tac	cgc	cag	879
Glu	Asp	Glu	Met	Tyr	Lys	Ile	Leu	Leu	Asn	Asp	Tyr	Glu	Tyr	Arg	Gln	
			255					260					265			
aag	cag	atc	ctg	ctg	gag	aat	gcg	gag	ctg	aag	aag	gtc	ctc	cag	cag	927
Lys	Gln	Ile	Leu	Leu	Glu	Asn	Ala	Glu	Leu	Lys	Lys	Val	Leu	Gln	Gln	
		270					275					280				
atg	aag	aaa	gag	atg	atc	tct	ctc	ctt	tct	cct	caa	aag	aag	aaa	ccc	975
Met	Lys	Lys	Glu	Met	Ile	Ser	Leu	Leu	Ser	Pro	Gln	Lys	Lys	Lys	Pro	
	285					290					295					
aga	gaa	aga	gca	gag	gac	agc	aca	ggc	act	gtt	gtc	atc	tcc	gat	gta	1023
Arg	Glu	Arg	Ala	Glu	Asp	Ser	Thr	Gly	Thr	Val	Val	Ile	Ser	Asp	Val	
300					305					310					315	
gaa	gac	gac	gct	ggg	gag	ctg	agc	aga	gat	ggg	gtg	tgg	agc	ctt	tcc	1071
Glu	Asp	Asp	Ala	Gly	Glu	Leu	Ser	Arg	Asp	Gly	Val	Trp	Ser	Leu	Ser	
				320					325					330		
tgt	gac	act	gtc	agg	gag	cag	ctt	aca	aac	agc	atc	agg	aag	cag	tgg	1119
Cys	Asp	Thr	Val	Arg	Glu	Gln	Leu	Thr	Asn	Ser	Ile	Arg	Lys	Gln	Trp	
			335					340					345			
aga	att	ctg	aaa	agc	cat	gtg	gaa	aaa	ctt	gat	aac	caa	gct	tca	aag	1167
Arg	Ile	Leu	Lys	Ser	His	Val	Glu	Lys	Leu	Asp	Asn	Gln	Ala	Ser	Lys	
		350					355					360				

gta cac tca gag ggc ttt cat gaa gag gac gtc atc tca cga caa gac	1215
Val His Ser Glu Gly Phe His Glu Glu Asp Val Ile Ser Arg Gln Asp	
365 370 375	
cat gag caa gag act gag aaa ctg gag ctg gag att gag cgg tgt aaa	1263
His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys	
380 385 390 395	
gag atg atc aag gct cag cag cag ctc tta cag caa cag ctg gcc act	1311
Glu Met Ile Lys Ala Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr	
400 405 410	
gcg tgt gat gac gac acc acc tca ctg ttg cga gac tgt tac ttg ctt	1359
Ala Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu	
415 420 425	
gaa gaa aag gaa cgc ctt aaa gaa gag tgg tcc ctt ttt aaa gag caa	1407
Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp Ser Leu Phe Lys Glu Gln	
430 435 440	
aaa aag aat ttt gag aga gaa aga cga agc ttt aca gaa gct gct att	1455
Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile	
445 450 455	
cgc ttg ggg ttg gag aga aag gcg ttt gag gaa gag cga gcc agc tgg	1503
Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp	
460 465 470 475	
gtg aag cag cag ttt tta aac atg acg acc ttt gat cac cag aac tca	1551
Val Lys Gln Gln Phe Leu Asn Met Thr Thr Phe Asp His Gln Asn Ser	
480 485 490	
gaa aat gtg aaa ctt ttc agt gcc ttt tca gga agt tct gat cca gac	1599
Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp	
495 500 505	
aat ctt ata gtc cac cca cgg cca cgg caa aag aag cca cac agt gtc	1647
Asn Leu Ile Val His Pro Arg Pro Arg Gln Lys Lys Pro His Ser Val	
510 515 520	
gct aat ggg gtg cca gct tgc aca tcc aaa ctg gct aag tct ctt ccg	1695
Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Ala Lys Ser Leu Pro	
525 530 535	
acc tca cct tca gac ttc tgc ccg tct cgc tca tgt gtg tct gag cac	1743
Thr Ser Pro Ser Asp Phe Cys Pro Ser Arg Ser Cys Val Ser Glu His	
540 545 550 555	
agt ccc gtc agt gcg ctg act gtg act cct gaa gaa acc aaa ccg aat	1791
Ser Pro Val Ser Ala Leu Thr Val Thr Pro Glu Glu Thr Lys Pro Asn	
560 565 570	
gag gtt gga aga gaa agt acg gac cag aag tgg agc gtg gtg tcc aga	1839
Glu Val Gly Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Val Ser Arg	
575 580 585	
ccc agc tcc cgg gag ggt tgc tac ggt gga tgc tcc tcg gcc tac aca	1887
Pro Ser Ser Arg Glu Gly Cys Tyr Gly Gly Cys Ser Ser Ala Tyr Thr	
590 595 600	
agc tcc cac gtg gaa cga gat gac tta cca tag gtgctcgggc tgcagcgctg	1940

Ser Ser His Val Glu Arg Asp Asp Leu Pro
605 610

tccctggagtg catgagagga attgacacgg ggtgtagcat aaagtcagcc atctaccgta 2000
agatgtcggg gttatttggt tggacttccc agtctttccc caaagagctg aaacgcttta 2060
gaggatgcga aagctttggc tgtgtgttag taacagaagc ctctggctct gtgagtaaag 2120
gaatgtatgg tgtttggtgg gaaacaaaag cacgagaatg atttcctctt cgggtactg 2180
agaatagcac ttttagggac tgattcttgt aaacattaaa tttttgtccc aagtatgggt 2240
ggcattggaa gtttagtctt tacttgaatg tacactgtag atttttaaca aagcagttct 2300
atatttatta tgtttagtgt gattttggga ttacctcttt catatgtttt ctgcctgtac 2360
ataaatatac atgactatgt taagaggctt taaggtttaa aaatttcaca ccatgctcga 2420
gnatagcatt tcatgccaat taaaatgttt tcagtggcat ggtgtttaca gatgtgttag 2480
gaccactgcc acatgacagt taagatttta tttttaagcc atttgggcaa taaaaattca 2540
aagccacttc ataagctaag ttcagatagc taaaactact aacattacat ttttgagatt 2600
tataaagcat tatattttat tttatatatg tgactgttat aatttctaag aggaatgtgg 2660
attatgaagc aatgggggaa agacagaagt gactaatagt gcaagagcat tgggtgaagg 2720
gacggctgat gaggatatgg gagacctggg tgggtgatctt ttccttaccg acggtgcggt 2780
gcggcgatct ctgtaccgcc agggctttct atcattgcca atacttttgt aattaaagag 2840
attttcaact acataccact actaaagtaa gacagtgtaa aactttggct tttgtaattg 2900
acactctgga cactgggtgtg ttgttcattt ctagaacaat cgtaggctct tttctctgtt 2960
tctgctgcat gtttcttcat gagaagtatg ttactattga cagtaatgac actgacagtg 3020
actgtagacg taggcccaga cttctcctgg gtggattttc atccagcagc ttttaagtgc 3080
ctcgccctgc tcgtctctgc acatagccgc cgacacaagc cctcgcttga tgatgcagat 3140
agtcacatctg cctttctctc cccttgccct gctatgactg ttgcattaaa ttcac 3195

<210> 4
<211> 613
<212> PRT
<213> Rattus norvegicus

<400> 4

Met Gly Asp Trp Met Thr Val Thr Asp Pro Val Leu Cys Thr Glu Asn
1 5 10 15

Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser
20 25 30

Leu Tyr Ser Gln Gln Val Leu Cys Ser Ala Thr Pro Leu Ser Lys Asn
 35 40 45

Val His Gly Val Phe Ser Ala Phe Cys Thr Gly Glu Asn Ile Glu Gln
 50 55 60

Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
 65 70 75 80

Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Ser Ile
 85 90 95

Val Ala Leu Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
 100 105 110

Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
 115 120 125

Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
 130 135 140

Leu Glu Ala Ser Arg Arg Glu Met Ile Ser Leu Gln Glu Arg Asp Arg
 145 150 155 160

Gln Leu Gln Cys Lys Asn Arg Asn Leu His Gln Leu Leu Lys Asn Glu
 165 170 175

Lys Glu Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
 180 185 190

Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
 195 200 205

Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
 210 215 220

Ala Met Asp Val Leu Asn Tyr Val Gly Arg Val Asp Gly Lys Arg Gly
 225 230 235 240

Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
 245 250 255

Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Leu
 260 265 270

Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met

275		280		285
Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro Arg Glu Arg Ala Glu				
290		295		300
Asp Ser Thr Gly Thr Val Val Ile Ser Asp Val Glu Asp Asp Ala Gly				
305		310		315
Glu Leu Ser Arg Asp Gly Val Trp Ser Leu Ser Cys Asp Thr Val Arg				
		325		330
				335
Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser				
		340		345
				350
His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly				
		355		360
				365
Phe His Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr				
		370		375
				380
Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala				
385		390		395
				400
Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Ala Cys Asp Asp Asp				
		405		410
				415
Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg				
		420		425
				430
Leu Lys Glu Glu Trp Ser Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu				
		435		440
				445
Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu				
		450		455
				460
Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe				
465		470		475
				480
Leu Asn Met Thr Thr Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu				
		485		490
				495
Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His				
		500		505
				510
Pro Arg Pro Arg Gln Lys Lys Pro His Ser Val Ala Asn Gly Val Pro				
		515		520
				525

Ala Cys Thr Ser Lys Leu Ala Lys Ser Leu Pro Thr Ser Pro Ser Asp
 530 535 540

Phe Cys Pro Ser Arg Ser Cys Val Ser Glu His Ser Pro Val Ser Ala
 545 550 555 560

Leu Thr Val Thr Pro Glu Glu Thr Lys Pro Asn Glu Val Gly Arg Glu
 565 570 575

Ser Thr Asp Gln Lys Trp Ser Val Val Ser Arg Pro Ser Ser Arg Glu
 580 585 590

Gly Cys Tyr Gly Gly Cys Ser Ser Ala Tyr Thr Ser Ser His Val Glu
 595 600 605

Arg Asp Asp Leu Pro
 610

<210> 5
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 5
 cgtaggagag tgacaggagc tg

22

<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 6
 ggttatcgag tttttctaca tgac

24

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 7
 cgtaggagag tgacaggagc tg

22

<210> 8
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> an artificially synthesized primer sequence

<400> 8
 ttctctgtttt tgcactgtag ctg

23

<210> 9
 <211> 626
 <212> PRT
 <213> Homo sapiens

<400> 9

Thr Ser Ser Ser Gly Ile Leu Ala Leu Glu Ile Ala Met Gly Asp Trp
 1 5 10 15

Met Thr Val Thr Asp Pro Gly Leu Ser Ser Glu Ser Lys Thr Ile Ser
 20 25 30

Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser Leu Tyr Ser Gln
 35 40 45

Gln Val Leu Cys Ser Ser Ile Pro Leu Ser Lys Asn Val His Ser Phe
 50 55 60

Phe Ser Ala Phe Cys Thr Glu Asp Asn Ile Glu Gln Ser Ile Ser Tyr
 65 70 75 80

Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser Leu Tyr Glu Glu
 85 90 95

Ser Lys Gly Lys Glu Thr Lys Arg Glu Leu Asn Ile Val Ala Val Leu
 100 105 110

Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys Asn Leu Leu Ala
 115 120 125

Gln Glu Asn Val Glu Thr Gln Asn Leu Lys Leu Gly Ser Asp Met Asp
 130 135 140

His Leu Gln Ser Cys Tyr Ser Lys Leu Lys Glu Gln Leu Glu Thr Ser
 145 150 155 160

Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg Gln Leu Gln Cys

				165					170					175		
Lys	Asn	Arg	Asn	Leu	His	Gln	Leu	Leu	Lys	Asn	Glu	Lys	Asp	Glu	Val	
			180					185					190			
Gln	Lys	Leu	Gln	Asn	Ile	Ile	Ala	Ser	Arg	Ala	Thr	Gln	Tyr	Asn	His	
		195					200					205				
Asp	Met	Lys	Arg	Lys	Glu	Arg	Glu	Tyr	Asn	Lys	Leu	Lys	Glu	Arg	Leu	
	210					215					220					
His	Gln	Leu	Val	Met	Asn	Lys	Lys	Asp	Lys	Lys	Ile	Ala	Met	Asp	Ile	
225					230					235					240	
Leu	Asn	Tyr	Val	Gly	Arg	Ala	Asp	Gly	Lys	Arg	Gly	Ser	Trp	Arg	Thr	
				245					250					255		
Gly	Lys	Thr	Glu	Ala	Arg	Asn	Glu	Asp	Glu	Met	Tyr	Lys	Ile	Leu	Leu	
			260					265					270			
Asn	Asp	Tyr	Glu	Tyr	Arg	Gln	Lys	Gln	Ile	Leu	Met	Glu	Asn	Ala	Glu	
		275					280					285				
Leu	Lys	Lys	Val	Leu	Gln	Gln	Met	Lys	Lys	Glu	Met	Ile	Ser	Leu	Leu	
	290					295					300					
Ser	Pro	Gln	Lys	Lys	Lys	Pro	Arg	Glu	Arg	Val	Asp	Asp	Ser	Thr	Gly	
305					310					315					320	
Thr	Val	Ile	Ser	Asp	Val	Glu	Glu	Asp	Ala	Gly	Glu	Leu	Ser	Arg	Glu	
				325					330					335		
Ser	Met	Trp	Asp	Leu	Ser	Cys	Glu	Thr	Val	Arg	Glu	Gln	Leu	Thr	Asn	
			340					345					350			
Ser	Ile	Arg	Lys	Gln	Trp	Arg	Ile	Leu	Lys	Ser	His	Val	Glu	Lys	Leu	
		355					360					365				
Asp	Asn	Gln	Val	Ser	Lys	Val	His	Leu	Glu	Gly	Phe	Asn	Asp	Glu	Asp	
	370					375					380					
Val	Ile	Ser	Arg	Gln	Asp	His	Glu	Gln	Glu	Thr	Glu	Lys	Leu	Glu	Leu	
385					390					395					400	
Glu	Ile	Gln	Gln	Cys	Lys	Glu	Met	Ile	Lys	Thr	Gln	Gln	Gln	Leu	Leu	
				405					410					415		

Gln Gln Gln Leu Ala Thr Ala Tyr Asp Asp Asp Thr Thr Ser Leu Leu
 420 425 430

Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp
 435 440 445

Ser Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser
 450 455 460

Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu
 465 470 475 480

Glu Glu Arg Ala Ser Trp Leu Lys Gln Gln Phe Leu Asn Met Thr Thr
 485 490 495

Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu Phe Ser Ala Phe Ser
 500 505 510

Gly Ser Ser Asp Trp Asp Asn Leu Ile Val His Ser Arg Gln Pro Gln
 515 520 525

Lys Lys Pro His Ser Val Ser Asn Gly Ser Pro Val Cys Met Ser Lys
 530 535 540

Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr Ser Asp Phe Cys Gln
 545 550 555 560

Thr Arg Ser Cys Ile Ser Glu His Ser Ser Ile Asn Val Leu Asn Ile
 565 570 575

Thr Ala Glu Glu Ile Lys Pro Asn Gln Val Gly Gly Glu Cys Thr Asn
 580 585 590

Gln Lys Trp Ser Val Ala Ser Arg Pro Gly Ser Gln Glu Gly Cys Tyr
 595 600 605

Ser Gly Cys Ser Leu Ser Tyr Thr Asn Ser His Val Glu Lys Asp Asp
 610 615 620

Leu Pro
 625